CLAIMS

1. Nucleic acid fragment, characterized in that it comprises a nucleic acid sequence coding for an androctonine.

2. Nucleic acid fragment according to claim 1, characterized in that it is a sequence of DNA.

3. Nucleic acid fragment according to ~~either of claims 1 and 2~~, characterized in that the androctonine consists of a peptide which can be produced by and isolated from scorpions, in particular from the species *Androctonus australis*, the said peptide comprising at least 20 amino acids, preferably at least 25 amino acids, and 4 cysteine residues which form disulphide bridges between themselves.

4. Nucleic acid fragment according to ~~one of claims 1 to 3~~, characterized in that the androctonine essentially comprises the peptide sequence of general formula (I) below

Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae

(I)

in which

Xaa represents a peptide residue comprising at least 1 amino acid,

Xab represents a peptide residue of 5 amino acids,

Xac represents a peptide residue of 5 amino acids,

Xad represents a peptide residue of 3 amino acids, and

Xae represents a peptide residue comprising at least 1 amino acid.

5. Nucleic acid fragment according to claim 4, characterized in that Xab and/or Xad and/or Xae comprise at least one basic amino acid.

6. Nucleic acid fragment according to claim 5, characterized in that the basic amino acids are chosen from lysine, asparagine and homoasparagine.

7. Nucleic acid fragment according to ~~one of claims 4 to 6~~ claim 4, characterized in that

Xaa represents the peptide sequence Xaa'-Val, in which Xaa' represents NH_2 or a peptide residue comprising at least 1 amino acid, and/or

Xab represents the peptide sequence -Arg-Xab'-Ile, in which Xab' represents a peptide residue of 3 amino acids, and/or

Xac represents the peptide sequence -Arg-Xac'-Gly-, in which Xac' represents a peptide residue of 3 amino acids, and/or

Xad represents the peptide sequence -Tyr-Xad'-Lys, in which Xad' represents a peptide residue of 1 amino acid, and/or

Xae represents the peptide sequence -Thr-Xae', in which Xae' represents COOH or a peptide residue comprising at least 1 amino acid.

8. Nucleic acid fragment according to claim 7, characterized in that

Xaa' represents the peptide sequence -Arg-Ser-, and/or

Xab' represents the peptide sequence -Gln-Ile-Lys-, and/or

Xac' represents the peptide sequence -Arg-Arg-Gly-, and/or

Xad' represents the peptide residue -Tyr-, and/or

Xae' represents the peptide sequence -Asn-Arg-Pro-Tyr.

9. Nucleic acid fragment according to ~~one of claims 1 to 8~~, characterized in that the androctonine is represented by the peptide sequence of 25 amino acids described by the sequence identifier No. 1 (SEQ ID NO. 1) and the homologous peptide sequences.

10. Nucleic acid fragment according to claim 9, characterized in that it is represented by the sequence identifier No. 1 (SEQ ID NO. 1), a homologous sequence or a sequence complementary to the said sequence, more particularly the coding portion of this SEQ ID NO. 1, corresponding to bases 1 to 75.

11. Nucleic acid fragment, characterized in that it comprises a nucleic acid sequence coding for a "peptide-androctonine" or "androctonine-peptide", advantageously "peptide-androctonine", fusion peptide, the androctonine being defined according to ~~one of claims 1 to 9~~.

12. Nucleic acid fragment according to claim 11, characterized in that the peptide fused to androctonine is a signal peptide or a transit peptide.

13. Nucleic acid fragment according to claim 12, characterized in that the transit peptide is a chloroplast-addressing signal or a mitochondrion-addressing signal.

14. Nucleic acid fragment according to claim 12, characterized in that the signal peptide is an N-terminal signal or "prepeptide", optionally in combination with a signal responsible for retaining the protein in the endoplasmic reticulum, or a vacuole-addressing peptide or "propeptide".

15. Nucleic acid fragment according to claim 14, characterized in that the signal peptide is the signal peptide of the tobacco PR-1α gene.

16. Nucleic acid fragment according to claim 15, characterized in that the "peptide-androctonine" fusion peptide is represented by the sequence identifier No. 3 (SEQ ID NO. 3).

17. Nucleic acid fragment according to claim 16, characterized in that the coding sequence is represented by the sequence identifier No. 3 (SEQ ID NO. 3), a homologous sequence or a complementary sequence, more particularly the coding portion of this SEQ ID NO. 3, corresponding to bases 12 to 176 of this sequence.

18. "Peptide-androctonine" or "androctonine-peptide", preferably "peptide-androctonine", fusion protein, characterized in that it is defined according to ~~claims 11 to 16~~ claim 11.

19. Chimeric gene comprising a coding sequence and heterologous regulation elements in positions 5' and 3' which can function in a host organism, in particular plant cells or plants, these

elements being functionally linked to the said coding sequence, characterized in that the said coding sequence comprises at least one DNA fragment coding for androctonine as defined according to ~~claims 1 to 17~~.

20. Chimeric gene according to claim 19, characterized in that the host organism is chosen from bacteria, for example *E. coli*, yeasts, in particular yeasts of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, a baculovirus, and plant cells and plants.

21. Chimeric gene according to ~~either of claims 19 and 20~~, characterized in that it is combined with a selection marker adapted to the transformed host organism.

22. Cloning or expression vector for the transformation of a host organism, characterized in that it comprises at least one chimeric gene as defined according to ~~claims 19 to 21~~.

23. Process for transforming host organisms, in particular plant cells, by incorporating at least one nucleic acid fragment or one chimeric gene as defined in ~~claims 19 to 21~~.

24. Process according to claim 23, characterized in that the chimeric gene is incorporated by means of ~~the vector according to claim 22~~.

25. Process according to ~~either of claims 23 and 24~~, characterized in that the host organism is chosen from bacteria, for example *E. coli*, yeasts, in

particular yeasts of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, a baculovirus, and plant cells and plants.

26. Process according to claim 25, characterized in that the host organism is a plant cell.

27. Process according to claim 26, characterized in that plants are regenerated from transformed plant cells.

28. Transformed host organism, in particular plant cell or plant, characterized in that it comprises a chimeric gene defined according to ~~one of claims 19 to 21~~ claim 19.

29. Host organism according to claim 28, characterized in that it is chosen from bacteria, for example *E. coli*, yeasts, in particular yeasts of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, a baculovirus, and plant cells and plants.

30. Plants, characterized in that they comprise transformed plant cells according to claim 29.

31. Plant according to claim 30, characterized in that it is regenerated from transformed plant cells.

32. Plant, characterized in that it is obtained from the cultivating and/or crossing of the regenerated plants according to claim 31.

33. Plant according to ~~one of claims 30 to~~ claim 30

~~32~~, characterized in that it is chosen from corn, wheat, rapeseed, soybean, rice, sugar cane, beetroot, tobacco and cotton.

34. Plant according to ~~one of claims 30 to 33~~ Claim 30, characterized in that it is resistant to fungal diseases such as those caused by *Cercospora*, in particular *Cercospora beticola*, *Cladosporium*, in particular *Cladosporium herbarum*, *Fusarium*, in particular *Fusarium culmorum* or *Fusarium graminearum*, or by *Phytophthora*, in particular *Phytophthora cinnamomi*.

35. Plant seeds according to ~~one of claims 30 to 34~~ Claim 30.

36. Process for cultivating transformed plants according to ~~one of claims 30 to 34, or obtained by the process according to claim 27~~ Claim 30, the said process consisting in planting the seeds of the said transformed plants in an area of a cultivation environment, in particular a field, which is suitable for cultivating the said plants, in applying an agrochemical composition to the said area, without substantially affecting the said transformed seeds or plants, and then in harvesting the plants cultivated when they reach the desired maturity, and optionally in separating the seeds from the harvested plants.

37. Process according to claim 36, characterized in that the agrochemical composition comprises at least one active product having at least a

fungicidal and/or bactericidal activity.

38. Process according to claim 37, characterized in that the active product has an activity complementary to that of the androctonine produced by the transformed plants.

39. Process for preparing ~~the~~ androctonine ~~defined according to one of claims 1 to 29~~, comprising the steps of cultivating the transformed host organism ~~defined according to either of claims 28 and 29~~ in an appropriate cultivation environment, followed by the extraction and total or partial purification of the androctonine obtained.